

SEQUENCE SUBMISSION

5 SEQ ID NO: 1 is a mouse 312C2 nucleic acid sequence.
SEQ ID NO: 2 is a mouse 312C2 amino acid sequence.
SEQ ID NO: 3 is a human 312C2 nucleic acid sequence.
SEQ ID NO: 4 is a human 312C2 amino acid sequence.
SEQ ID NO: 5 is a reverse translation sequence.
SEQ ID NO: 6 is clone A8 amino acid sequence.
10 SEQ ID NO: 7 is clone A5 amino acid sequence.
SEQ ID NO: 8 is clone G10 amino acid sequence.

SEQUENCE LISTING

15 (1) GENERAL INFORMATION:

- (i) APPLICANT: Gorman, Daniel M.
Randall, Troy D.
Zlotnik, Albert
- 20 (ii) TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related Reagents
- (iii) NUMBER OF SEQUENCES: 9
- 25 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
(C) CITY: Palo Alto
30 (D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1104
- (v) COMPUTER READABLE FORM:
35 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 40 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US Not yet assigned
(B) FILING DATE: August 14, 1997
(C) CLASSIFICATION:
- 45 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/023,419
(B) FILING DATE: 16-AUG-1996
- (vii) PRIOR APPLICATION DATA:
50 (A) APPLICATION NUMBER: US 60/027,901
(B) FILING DATE: 07-OCT-1996
- (viii) ATTORNEY/AGENT INFORMATION:
55 (A) NAME: Ching, Edwin P.
(B) REGISTRATION NUMBER: 34,090
(C) REFERENCE/DOCKET NUMBER: DX0612K1
- (ix) TELECOMMUNICATION INFORMATION:
60 (A) TELEPHONE:
(B) TELEFAX:

08914423-081497

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1073 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 68..754
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20	CTCGAGATCC ATTGTGCTGG AAAGGGAACCT CCTGAAATCA GCCGACAGAA GACTCAGGAG	60
	AAGCACT ATG GGG GCA TGG GCC ATG CTG TAT GGA GTC TCG ATG CTC TGT	109
	Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys	
25	1 5 10	
	GTG CTG GAC CTA GGT CAG CCG AGT GTA GTT GAG GAG CCT GGC TGT GGC	157
	Val Leu Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly	
	15 20 25 30	
30	CCT GGC AAG GTT CAG AAC GGA AGT GGC AAC AAC ACT CGC TGC TGC AGC	205
	Pro Gly Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser	
	35 40 45	
35	CTG TAT GCT CCA GGC AAG GAG GAC TGT CCA AAA GAA AGG TGC ATA TGT	253
	Leu Tyr Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys	
	50 55 60	
	GTC ACA CCT GAG TAC CAC TGT GGA GAC CCT CAG TGC AAG ATC TGC AAG	301
40	Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys	
	65 70 75	
	CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGG GAT ATT	349
	His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile	
45	80 85 90	
	GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA	397
	Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala	
	95 100 105 110	
50	GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA	445
	Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly	
	115 120 125	
55	TTT CTC ACC ATG TTC CCT GGG AAC AAG ACC CAC AAT GCT GTG TGC ATC	493
	Phe Leu Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile	
	130 135 140	
60	CCG GAG CCA CTG CCC ACT GAG CAA TAC GGC CAT TTG ACT GTC ATC TTC	541
	Pro Glu Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe	

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145 150 155

5 CTG GTC ATG GCT GCA TGC ATT TTC TTC CTA ACC ACA GTC CAG CTC GGC 589
Leu Val Met ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly
160 165 170

10 CTG CAC ATA TGG CAG CTG AGG AGG CAA CAC ATG TGT CCC CGA GAG ACC 637
Leu His Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr
175 180 185 190

CAG CCA TTC GCG GAG GTG CAG TTG TCA GCT GAG GAT GCT TGC AGC TTC 685
Gln Pro Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe
195 200 205

15 CAG TTC CCT GAG GAG GAA CGC GGG GAG CAG ACA GAA GAA AAG TGT CAT 733
Gln Phe Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His
210 215 220

20 CTG GGG GGT CGG TGG CCA TGAGGCCTGG TCTTCCTCTG TGCCCCAAGC 781
Leu Gly Gly Arg Trp Pro
225

CAGACGCTAC AAGACTTGCC CAGCTATACC CTTGGTGAGA GCAGGGGCCA TGCTCTGCAC 841

25 CCTTCCCTGG GCCTGGCCCT GCTCCCCTCA ACAGTGGCGG AAGTGGGTGT ATGAGAGCGG 901

TGAGTTACGA TTGGGCCCTA TGGCTGCCTT TCTCATTTGA CAGCTCTGTT GGAGTAGGGT 961

CTTTGGGCCC ACCAAGAGCA CCACGTTTAG CACAAGATCT TGTACAAGAA TAAATACTTG 1021

30 TTTAGTAACC TGAAAAAAAAA AAAAAAAGG GCGGCCGCGG AGGCCGAATT CC 1073

(2) INFORMATION FOR SEQ ID NO:2:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu
1 5 10 15

45 Asp Leu Gly Gln Pro Ser Val Val Glu Pro Gly Cys Gly Pro Gly
20 25 30

Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr
35 40 45

Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr
50 55 60

55 Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr
65 70 75 80

Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile Val Phe
85 90 95

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Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala Gly Arg
 100 105 110
 5 Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly Phe Leu
 115 120 125
 Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile Pro Glu
 130 135 140
 10 Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe Leu Val
 145 150 155 160
 Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly Leu His
 165 170 175
 15 Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr Gln Pro
 180 185 190
 Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe Gln Phe
 195 200 205
 20 Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His Leu Gly
 210 215 220
 25 Gly Arg Trp Pro
 225

(2) INFORMATION FOR SEQ ID NO:3:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1006 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 35 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

45 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..723

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

45 ATG GCA CAG CAC GGG GCG ATG GGC GCG TTT CGG GCC CTG TGC GGC CTG 48
 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
 1 5 10 15
 50 GCG CTG CTG TGC GCG CTC AGC CTG GGT CAG CGC CCC ACC GGG GGT CCC 96
 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
 20 25 30
 55 GGG TGC GGC CCT GGG CGC CTC CTG CTT GGG ACG GGA ACG GAC GCG CGC 144
 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
 35 40 45
 TGC TGC CGG GTT CAC ACG ACG CGC TGC TGC CGC GAT TAC CCC GGC GAG 192
 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
 50 55 60
 60

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	GAG	TGC	TGT	TCC	GAG	TGG	GAC	TGC	ATG	TGT	GTC	CAG	CCT	GAA	TTC	CAC	240
	Glu	Cys	Cys	Ser	Glu	Trp	Asp	Cys	Met	Cys	Val	Gln	Pro	Glu	Phe	His	
	65					70					75					80	
5																	
	TGC	GGA	GAC	CCT	TGC	TGC	ACG	ACC	TGC	CGG	CAC	CAC	CCT	TGT	CCC	CCA	288
	Cys	Gly	Asp	Pro	Cys	Cys	Thr	Thr	Cys	Arg	His	His	Pro	Cys	Pro	Pro	
					85					90					95		
10																	
	GGC	CAG	GGG	GTA	CAG	TCC	CAG	GGG	AAA	TTC	AGT	TTT	GGC	TTC	CAG	TGT	336
	Gly	Gln	Gly	Val	Gln	Ser	Gln	Gly	Lys	Phe	Ser	Phe	Gly	Phe	Gln	Cys	
				100					105					110			
15																	
	ATC	GAC	TGT	GCC	TCG	GGG	ACC	TTC	TCC	GGG	GGC	CAC	GAA	GGC	CAC	TGC	384
	Ile	Asp	Cys	Ala	Ser	Gly	Thr	Phe	Ser	Gly	Gly	His	Glu	Gly	His	Cys	
			115					120					125				
20																	
	AAA	CCT	TGG	ACA	GAC	TGC	ACC	CAG	TTC	GGG	TTT	CTC	ACT	GTG	TTC	CCT	432
	Lys	Pro	Trp	Thr	Asp	Cys	Thr	Gln	Phe	Gly	Phe	Leu	Thr	Val	Phe	Pro	
		130						135					140				
25																	
	GGG	AAC	AAG	ACC	CAC	AAC	GCT	GTG	TGC	GTC	CCA	GGG	TCC	CCG	CCG	GCA	480
	Gly	Asn	Lys	Thr	His	Asn	Ala	Val	Cys	Val	Pro	Gly	Ser	Pro	Pro	Ala	
	145					150					155					160	
30																	
	GAG	CCG	CTT	GGG	TGG	CTG	ACC	GTC	GTC	CTC	CTG	GCC	GTG	GCC	GCC	TGC	528
	Glu	Pro	Leu	Gly	Trp	Leu	Thr	Val	Val	Leu	Leu	Ala	Val	Ala	Ala	Cys	
					165					170					175		
35																	
	GTC	CTC	CTC	CTG	ACC	TCG	GCC	CAG	CTT	GGA	CTG	CAC	ATC	TGG	CAG	CTG	576
	Val	Leu	Leu	Leu	Thr	Ser	Ala	Gln	Leu	Gly	Leu	His	Ile	Trp	Gln	Leu	
				180					185					190			
40																	
	AGG	AGT	CAG	TGC	ATG	TGG	CCC	CGA	GAG	ACC	CAG	CTG	CTG	CTG	GAG	GTG	624
	Arg	Ser	Gln	Cys	Met	Trp	Pro	Arg	Glu	Thr	Gln	Leu	Leu	Leu	Glu	Val	
			195					200					205				
45																	
	CCG	CCG	TCG	ACC	GAA	GAC	GCC	AGA	AGC	TGC	CAG	TTC	CCC	GAG	GAA	GAG	672
	Pro	Pro	Ser	Thr	Glu	Asp	Ala	Arg	Ser	Cys	Gln	Phe	Pro	Glu	Glu	Glu	
		210					215					220					
50																	
	CGG	GGC	GAG	CGA	TCG	GCA	GAG	GAG	AAG	GGG	CGG	CTG	GGA	GAC	CTG	TGG	720
	Arg	Gly	Glu	Arg	Ser	Ala	Glu	Glu	Lys	Gly	Arg	Leu	Gly	Asp	Leu	Trp	
	225					230					235				240		
55																	
	GTG	TGAGCCTGGC	CGTCCTCCGG	GGCCACCGAC	CGCAGCCAGC	CCCTCCCCAG											773
	Val																
60																	
	GAGCTCCCCA	GGCCGCAGGG	GCTCTGCGTT	CTGCTCTGGG	CCGGGCCCTG	CTCCCCTGGC											833
	AGCAGAAGTG	GGTGCAGGAA	GGTGGCAGTG	ACCAGCGCCC	TGACCATGC	AGTTCGGCGG											893
	CCGCTCTAAA	GGATCCAAGC	TTACGTACGC	GTGCATGCGA	CGTCATAGCT	CTTCTATAGT											953
	GTCACCTAAA	TTCAATTAC	TGGCCGTCGT	TTACAACGT	CCTGACTGGG	AAA											1006

(2) INFORMATION FOR SEQ ID NO:4:

60

454427680

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

10 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
1 5 10 15
Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
20 25 30
15 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
35 40 45
20 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
50 55 60
Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
65 70 75 80
25 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
85 90 95
Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
100 105 110
30 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
115 120 125
35 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
130 135 140
Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
145 150 155 160
40 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
165 170 175
Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
180 185 190
45 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
195 200 205
50 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
210 215 220
Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
225 230 235 240
55 Val

(2) INFORMATION FOR SEQ ID NO:5:

60

000142-081497

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCNCARC AYGGNGCNAT GGGNGCNTTY MGNGCNYTNT GYGGNYTNGC NYTNYTNTGY 60
GCNYTNWSNY TNGGNCARMG NCCNACNGGN GGNCNGGNT GYGGNCCNGG NMGNNTNYTN 120
YTNGGNACNG GNACNGAYGC NMGNTGYTGY MGNGTNCAYA CNACNMGNTG YTG YMGNGAY 180
TAYCCNGGNG ARGARTGYTG YWSNGARTGG GAYTGYATGT GYGTNCARCC NGARTTYCAY 240
TGYGGNGAYC CNTGYTGYAC NACNTGYMGN CAYCAYCCNT GYCCNCCNGG NCARGGNGTN 300
CARWSNCARG GNAARTTYWS NTTYGGNTTY CARTGYATHG AYTGYGCNWS NGGNACNTTY 360
WSNGGNGGNC AYGARGGNA YTG YAAARCCN TGGACNGAYT GYACNCARTT YGGNTTYTNY 420
ACNGTNTTYC CNGGNAAYAA RACNCAYAA GCGTNTTGYG TNCCNGGNWS NCCNCCNGCN 480
GARCCNYTNG GNTGGYTNAC NGTNGTNYTN YTNGCNGTNG CNGCNTGYGT NYTNYTNYTN 540
ACNWSNGCNC ARYTNGGNYT NCAYATHTGG CARYTNMGNW SNCARTGYAT GTGGCCNMGN 600
GARACNCARY TNYTNYTNGA RGTNCCNCCN WSNACNGARG AYGCNMGNWS NTGYCARTTY 660
CCNGARGARG ARMGNGGNGA RMGNWSNGCN GARGARAARG GNMGNYTNGG NGAYYTNTGG 720
GTN 723

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu
1 5 10 15
Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg
20 25 30

5 Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr
 35 40 45
 Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp
 50 55 60
 Asp Cys Met Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys
 65 70 75 80
 10 Thr Thr Cys Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser
 85 90 95
 Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys Ile Asp Cys Ala Ser Gly
 100 105 110
 15 Thr Phe Ser Gly Gly His Glu Gly His Cys Lys Pro Trp Thr Asp Cys
 115 120 125
 20 Thr Gln Phe Gly Phe Leu Thr Val Phe Pro Gly Asn Lys Thr His Asn
 130 135 140
 Ala Val Cys Val Pro Gly Ser Pro Pro Ala Glu Pro Leu Gly Trp Leu
 145 150 155 160
 25 Thr Val Val Leu Leu Ala Val Ala Ala Cys Val Leu Leu Leu Thr Ser
 165 170 175
 Ala Gln Leu Gly Leu His Ile Trp Gln Leu Arg Lys Thr Gln Leu Leu
 180 185 190
 30 Leu Glu Val Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro
 195 200 205
 35 Glu Glu Glu Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly
 210 215 220
 Asp Leu Trp Val
 225

40 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

55 Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu
 1 5 10 15
 Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg
 20 25 30
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Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr
35 40 45

5 Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp
50 55 60

Asp Cys Met Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys
65 70 75 80

10 Thr Thr Cys Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser
85 90 95

Gln Gly Lys Ser Trp Arg Cys Leu Trp Glu Ser Thr Gln Ala Arg Gly
100 105 110

15 Ser Thr Arg Ala Arg Gly Arg Ala Arg Gly His Arg Cys Pro Ala Arg
115 120 125

20 Thr Cys Gly Val Trp Gly Pro Glu Ser Cys Glu Ala Gly Gln Ala Arg
130 135 140

Pro Cys Ser Gly Thr Thr Gly His Glu Ala Leu Gly Val Ser Cys Pro
145 150 155 160

25 Cys Phe Leu Ser Leu Gly Phe Ser Ile Gln His Glu Gly Cys Glu Asn
165 170 175

Pro Ala Gly Arg Trp Gly Arg Val Pro Gly Ala Val Trp Leu Ser Gly
180 185 190

30 Pro Gly His Pro Ser Cys Leu Ser Ser Pro His Thr Glu Arg Ala Cys
195 200 205

35 Pro Val Pro Pro Gly Val Leu Ser Gly Ala Trp Gly Cys Thr Leu Phe
210 215 220

Trp Lys Glu Gln Leu Lys Ser Ser
225 230

40 (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

55 Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu
1 5 10 15

Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg
20 25 30

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Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr
35 40 45

5 Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp
50 55 60

Asp Cys Met Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys
65 70 75 80

10 Thr Thr Cys Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser
85 90 95

Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys Ile Asp Cys Ala Ser Gly
100 105 110

15 Thr Phe Ser Gly Gly His Glu Gly His Cys Lys Pro Trp Thr Asp Cys
115 120 125

20 Thr Gln Phe Gly Phe Leu Thr Val Phe Pro Gly Asn Lys Thr His Asn
130 135 140

Ala Val Cys Val Pro Gly Ser Pro Pro Ala Glu Pro Leu Gly Trp Leu
145 150 155 160

25 Thr Val Val Leu Leu Ala Val Ala Ala Cys Val Leu Leu Leu Thr Ser
165 170 175

Ala Gln Leu Gly Leu His Ile Trp Gln Leu Arg Ser Gln Cys Met Trp
180 185 190

30 Pro Arg Gly Leu Ser Gln Pro Gly Ala Gly Arg Trp Glu His Gly Cys
195 200 205

Leu Leu Thr Val Ala Pro Leu Gln Arg Pro Ser Cys Cys Trp Arg Cys
210 215 220

Arg Arg Arg Pro Lys Thr Pro Glu Ala Ala Ser Ser Pro Arg Lys Ser
225 230 235 240

40 Gly Ala Ser Asp Arg Gln Arg Arg Arg Gly Gly Trp Glu Thr Cys Gly
245 250 255

Cys Glu Pro Gly Arg Pro Pro Gly Pro Pro Thr Ala Ala Ser Pro Ser
260 265 270

45 Pro Gly Ala Pro Gln Ala Ala Gly Ala Leu Arg Ser Ala Leu Gly Arg
275 280 285

Ala Leu Leu Pro Trp Gln Gln Lys Trp Val Gln Glu Gly Gly Ser Asp
290 295 300

Gln Arg Pro Gly Pro Cys Ser
305 310

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000142-0049